



**FIG S1** Determination of *S. pyogenes* genetic lineages. Initial (A) and refined (B) model fits for hierarchical density-based spatial clustering of 26,465 *S. pyogenes* pseudo core genomes. Pseudo core genomes were generated based on 415,239 core SNPs identified relative to the genome of reference M89 strain MGAS23530. Population partitions were determined using PopPUNK v 2.3.0.